

Human 23565

Carboxypeptidase Activation Peptide Domain

Zinc Carboxypeptidase Domain

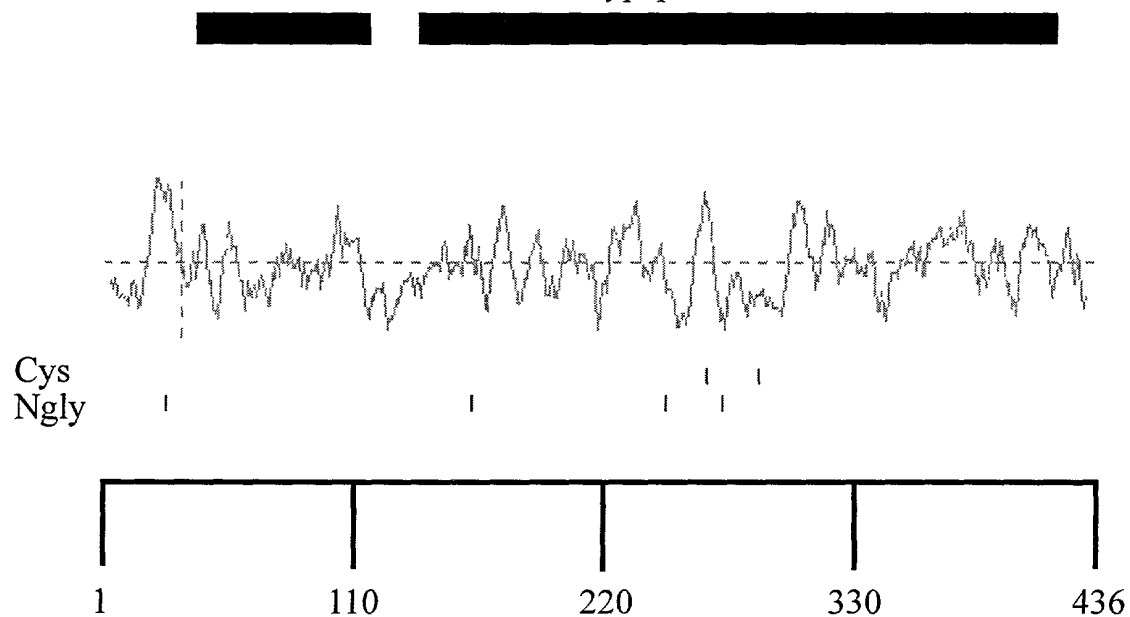


Fig. 1

Zn_carbOpept: domain 1 of 1, from 139 to 419; score 413.7, E = 1.7e-120

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*-->YhnleeiyawldllvsnfPdLvskvsiGksyeGRdlkvLkisdnpat
Yh+leeiy+w+D+ v ++ d+vsk++iG+s++ + vLK+s++
YHTLEEIYSWIDNFVMEHSDIVSKIQIGNSFENQISILVLFSTG-- 182

genePevfavagWiHAREwvtsAtllwlkelvanYgsDktitklldgld
g++ P++++++g iH+REw+t At w++++++v++Yg D t++l+ +d
183 GSRHPAIWIDTG-IHSREWITHTATGIWTANKIVSDYGKDRVLTIDILNAMD 231

lfyilpvfnpDGyaYsittdsYrmWRKtRspnagsfcvGtDpNRNWyawq
++i v+NpDG+a++++ + R+WRK+ s ++g fc+G+D+NRNW +++
232 -IFIELVTNPdGFAFTHSMN--RLWRKNKSIRPGIFCIGVDLNRNWKSGF 278

ggmgassysPcSetYeGtapfSepEtKavedfirsWlGGGknIkayItf
gg g +s +PcSetY+G+ p Se E++a++++fi ++ n ka+I++
279 GGNGSNS-NPCSETYHGPPSPQSESEVAIVNFITAHG-----NFKALISI 322

HsYSqllyPYgydynlnpdandldelsdlkiaadal sarhgyYtlglp
HsYSq+l+yPYg+ + + ++ +l+ +l+ k a+ al hg Y g +
323 HSYSQMLMYPYGRLLLEPVSNQRELYDLA--KDAVEALYKVHGIEYIFG-S 369

gsstIYPasAGGsdDwaydvgiikyafteLrpdtdgsyGnPCFl1PeeqI
+s+t+Y+as G + Dwayd g ikyaf fElr dtg yG Fl1P++qI
370 ISTTLYVAS-GITVDWAYDSG-IKYAFSFE LR-DTGQYG---FLLPATQI 413

iptgsee<-* (SEQ ID NO:4)
ipt++ e
414 IPTAQ-E 419
Fbh23565f1

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Fig. 2A

zn_carb: domain 1 of 1, from 139 to 419: score 401.8, E = 6.7e-117

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*->YhsyeeinawlddLarnyPdltSVslisigksyeGRpikviki....
Yh++++ei++w+d+ ++++ d+ Vs i+iG+s+++ i+vlk+++++
YHTLEEIYSWIDNFMVMEHSDI--VSKIQIGNSFENQSILVLKFstgg 183

..kpavfidagiHAREWiapatalylinqLltneteYskdpddegsvtkl
++ pa++id giH REWi+ at +++n+++++ Y+kd ++ t++
184 srHPAIWIDTGIHSREWITHTATGIWTANKIVSD--YGKD-RV---LTDI 226

LdkldwyivPvmNPDGYeythtstdRlWRKnRspngasgsqgtwynCyGv
L+ +d++i v+NPDG+++th+ ++RlWRKn s + C+Gv
227 LNAMDIFIELVTNPDGFATHS-MNRLWRKNKSIRPG-----IF-CIGV 268

DLNRNfdhnWgeigGssslpCsetYaGsspseWEpEtkaIldfilsne
DLNRN+ ++ +g+ Gs+s+pCsetY+G+sp+S E E+ a+ +fi+ +
269 DLNRNWKSG-FGGN-GSNSNPCSETYHGFPQS--ESEVAAIVNFITAH- 313

igkgrikayislHsysqllyPyGytnatvppngedlhkevakaakaig
g++ka is+Hsysq+l+yPyG + ++n+++l ++ak a+++a+
314 ---GNFKALISHSYSQMLMYPYGRLL-EPVSNQRELY-DLAKDAVEALY 358

dyYfgGtlytpGssadpdliditlypasGgsdDwaygtlkgvkysytiEL
+++ G Y G s+++ tly asG++ Dway+ + +ky++ +EL
359 KVH--GIEYIFG-SIST-----TLVVASGITVDWAYDSG--IKYAFSFE 398

rdtgddagrygFlLppscvkvrmegiipgteE<-* (SEQ ID NO:5)
rdt g+yGFlLp+ qiipgt+ E
399 RDT----GQYGFLLP-----TQIIPTAQE 419

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Fig. 2B

Propep_M14: domain 1 of 1, from 41 to 118: score 100.3, E = 3.8e-26

*->qVlrvkvadedQvk11kdLentehleLDFWkpdSATpikpgstvDfr
qVlrv + de+Q++11 dLe ++ DFW++ p++p +vD r
Fbh23565f1 41 QVLRVLAKDEKQLSLGLGDLEGLKPQKVDFWRG----PARPSLPVDMR 83

VpaediqavksfLeqsgIhYevlIeDVqeLleeqf<-* (SEQ ID NO:6)
Vp++++ ++k+ Le++g+ Y+++I D q+lL+e++
Fbh23565f1 84 VPFSELKDIKAYLIESHGLAYSIMIKDIQVLLDEER 118

Fig. 3